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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/653,961

DATE: 09/19/2000  
 TIME: 19:10:43

Input Set : A:\95-97.app  
 Output Set: N:\CRF3\09192000\I653961.raw

3 <110> APPLICANT: Wu, Guang-Jer  
 5 <120> TITLE OF INVENTION: Diagnostic for Metastatic Prostate Cancer  
 7 <130> FILE REFERENCE: 95-97  
 C---> 9 <140> CURRENT APPLICATION NUMBER: US/09/653,961  
 10 <141> CURRENT FILING DATE: 2000-09-01  
 12 <150> PRIOR APPEICATION NUMBER: US 60/076,664  
 13 <151> PRIOR FILING DATE: 1998-03-03  
 15 <150> PRIOR APPLICATION NUMBER: PCT US99/04850  
 16 <151> PRIOR FILING DATE: 1999-03-02  
 18 <160> NUMBER OF SEQ ID NOS: 16  
 20 <170> SOFTWARE: PatentIn Ver. 2.0  
 22 <210> SEQ ID.NO: 1  
 23 <211> LENGTH: 1950  
 24 <212> TYPE: DNA  
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 27 <220> FEATURE:  
 28 <221> NAME/KEY: CDS  
 29 <222> LOCATION: (1)..(1938)  
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 34 1 5 10 15  
 36 tgc tgt cct cgc gtc gcg ggt gtg ccc gga gag gct gag cag cct gcg 96  
 37 Cys Cys Pro Arg Val Ala Gly Val Pro Gly Glu Ala Glu Gln Pro Ala  
 38 20 25 30  
 40 cct gag ctg gtg gag gtg gaa gtg ggc agc aca gcc ctt ctg aag tgc 144  
 41 Pro Glu Leu Val Glu Val Glu Val Gly Ser Thr Ala Leu Leu Lys Cys  
 42 35 40 45  
 44 ggc ctc tcc cag tcc caa ggc aac ctc agc cat gtc gac tgg ttt tct 192  
 45 Gly Leu Ser Gln Ser Gln Gly Asn Leu Ser His Val Asp Trp Phe Ser  
 46 50 55 60  
 48 gtc cac aag gag aag cgg acg ctc atc ttc cgt gtg cgc cag ggc cag 240  
 49 Val His Lys Glu Lys Arg Thr Leu Ile Phe Arg Val Arg Gln Gly Gln  
 50 65 70 75 80  
 52 ggc cag agc gaa cct ggg gag tac gag cag cgg ctc agc ctc cag gac 288  
 53 Gly Gln Ser Glu Pro Gly Glu Tyr Glu Gln Arg Leu Ser Leu Gln Asp  
 54 85 90 95  
 56 aga ggg gct act ctg gcc ctg act caa gtc acc ccc caa gac gag cgc 336  
 57 Arg Gly Ala Thr Leu Ala Leu Thr Gln Val Thr Pro Gln Asp Glu Arg  
 58 100 105 110  
 60 atc ttc ttg tgc cag ggc aag cgc cct cgg tcc cag gag tac cgc atc 384  
 61 Ile Phe Leu Cys Gln Gly Lys Arg Pro Arg Ser Gln Glu Tyr Arg Ile  
 62 115 120 125  
 64 cag ctc cgc gtc tac aaa gct ccg gag gag cca aac atc cag gtc aac 432  
 65 Gln Leu Arg Val Tyr Lys Ala Pro Glu Glu Pro Asn Ile Gln Val Asn  
 66 130 135 140  
 68 ccc ctg ggc atc cct gtg aac agt aag gag cct gag gag gtc gct acc 480

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69 Pro Leu Gly Ile Pro Val Asn Ser Lys Glu Pro Glu Glu Val Ala Thr
70 145 150 155 160
72 tgt gta ggg agg aac ggg tac ccc att cct caa gtc atc tgg tac aag 528
73 Cys Val Gly Arg Asn Gly Tyr Pro Ile Pro Gln Val Ile Trp Tyr Lys
74 165 170 175
76 aat ggc cgg cct ctg aag gag gag aag aac cgg gtc cac att cag tcg 576
77 Asn Gly Arg Pro Leu Lys Glu Glu Lys Asn Arg Val His Ile Gln Ser
78 180 185 190
80 tcc cag act gtg gag tcg agt ggt ttg tac acc ttg cag agt att ctg 624
81 Ser Gln Thr Val Glu Ser Ser Gly Leu Tyr Thr Leu Gln Ser Ile Leu
82 195 200 205
84 aag gca cag ctg gtt aaa gaa gac aaa gat gcc cag ttt tac tgt gag 672
85 Lys Ala Gln Leu Val Lys Glu Asp Lys Asp Ala Gln Phe Tyr Cys Glu
86 210 215 220
88 ctc aac tac cgg ctg ccc agt ggg aac cac atg aag gag tcc agg gaa 720
89 Leu Asn Tyr Arg Leu Pro Ser Gly Asn His Met Lys Glu Ser Arg Glu
90 225 230 235
92 gtc acc gtc cct gtt ttc tac ccg aca gaa aaa gtg tgg ctg gaa gtg 768
93 Val Thr Val Pro Val Phe Tyr Pro Thr Glu Lys Val Trp Leu Glu Val
94 245 250 255
96 gag ccc gtg gga atg ctg aag gaa ggg gac cgc gtg gaa atc agg tgt 816
97 Glu Pro Val Gly Met Leu Lys Glu Gly Asp Arg Val Glu Ile Arg Cys
98 260 265 270
100 ttg gct gat ggc aac cct cca cca cac ttc agc atc agc aag cag aac 864
101 Leu Ala Asp Gly Asn Pro Pro Pro His Phe Ser Ile Ser Lys Gln Asn
102 275 280 285
104 ccc agc acc agg gag gca gag gaa gag aca acc aac gac aac ggg gtc 912
105 Pro Ser Thr Arg Glu Ala Glu Glu Glu Thr Thr Asn Asp Asn Gly Val
106 290 295 300
108 ctg gtg ctg gag cct gcc cgg aag gaa cac agt ggg cgc tat gaa tgt 960
109 Leu Val Leu Glu Pro Ala Arg Lys Glu His Ser Gly Arg Tyr Glu Cys
110 305 310 315
112 cag ggc ctg gac ttg gac acc atg ata tcg ctg ctg agt gaa cca cag 1008
113 Gln Gly Leu Asp Leu Asp Thr Met Ile Ser Leu Leu Ser Glu Pro Gln
114 325 330 335
116 gaa cta ctg gtg aac tat gtg tct gac gtc cga gtg agt ccc gca gcc 1056
117 Glu Leu Leu Val Asn Tyr Val Ser Asp Val Arg Val Ser Pro Ala Ala
118 340 345 350
120 cct gag aga cag gaa ggc agc agc ctc acc ctg acc tgt gag gca gag 1104
121 Pro Glu Arg Gln Glu Gly Ser Ser Leu Thr Leu Thr Cys Glu Ala Glu
122 355 360 365
124 agt agc cag gac ctc gag ttc cag tgg ctg aga gaa gag aca ggc cag 1152
125 Ser Ser Gln Asp Leu Glu Phe Gln Trp Leu Arg Glu Glu Thr Gly Gln
126 370 375 380
128 gtg ctg gaa agg ggg cct gtg ctt cag ttg cat gac ctg aaa cgg gag 1200
129 Val Leu Glu Arg Gly Pro Val Leu Gln Leu His Asp Leu Lys Arg Glu
130 385 390 395
132 gca gga ggc ggc tat cgc tgc gtg gcg tct gtg ccc agc ata ccc gga 1248
133 Ala Gly Gly Gly Tyr Arg Cys Val Ala Ser Val Pro Ser Ile Pro Gly

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134          405          410          415
136 ctg aac cgc aca cag ctg gtc aac gtg gcc att ttt ggc ccc cct tgg 1296
137 Leu Asn Arg Thr Gln Leu Val Asn Val Ala Ile Phe Gly Pro Pro Trp
138          420          425          430
140 atg gca ttc aag gag agg aag gtg tgg gtg aaa gag aat atg gtg ttg 1344
141 Met Ala Phe Lys Glu Arg Lys Val Trp Val Lys Glu Asn Met Val Leu
142          435          440          445
144 aat ctg tct tgt gaa gcg tca ggg cac ccc cgg ccc acc atc tcc tgg 1392
145 Asn Leu Ser Cys Glu Ala Ser Gly His Pro Arg Pro Thr Ile Ser Trp
146          450          455          460
148 aac gtc aac ggc acg gca agt gaa caa gac caa gat cca cag cga gtc 1440
149 Asn Val Asn Gly Thr Ala Ser Glu Gln Asp Gln Asp Pro Gln Arg Val
150 465          470          475          480
152 ctg agc acc ctg aat gtc ctc gtg acc ccg gag ctg ttg gag aca ggt 1488
153 Leu Ser Thr Leu Asn Val Leu Val Thr Pro Glu Leu Leu Glu Thr Gly
154          485          490          495
156 gtt gaa tgc acg gcc tcc aac gac ctg ggc aaa aac acc agc atc ctc 1536
157 Val Glu Cys Thr Ala Ser Asn Asp Leu Gly Lys Asn Thr Ser Ile Leu
158          500          505          510
160 ttc ctg gag ctg gtc aat tta acc acc ctc aca cca gac tcc aac aca 1584
161 Phe Leu Glu Leu Val Asn Leu Thr Thr Leu Thr Pro Asp Ser Asn Thr
162          515          520          525
164 acc act ggc ctc agc act tcc act gcc agt cct cat acc aga gcc aac 1632
165 Thr Thr Gly Leu Ser Thr Ser Thr Ala Ser Pro His Thr Arg Ala Asn
166          530          535          540
168 agc acc tcc aca gag aga aag ctg ccg gag agc cgg ggc gtg 1680
169 Ser Thr Ser Thr Glu Arg Lys Leu Pro Glu Pro Glu Ser Arg Gly Val
170 545          550          555          560
172 gtc atc gtg gct gtg att gtg tgc atc ctg gtc ctg gcg gtg ctg ggc 1728
173 Val Ile Val Ala Val Ile Val Cys Ile Leu Val Leu Ala Val Leu Gly
174          565          570          575
176 gct gtc ctc tat ttc ctc tat aag aag ggc aag ctg ccg tgc agg cgc 1776
177 Ala Val Leu Tyr Phe Leu Tyr Lys Lys Gly Lys Leu Pro Cys Arg Arg
178          580          585          590
180 tca ggg aag cag gag atc acg ctg ccc ccg tct cgt aag agc gaa ctt 1824
181 Ser Gly Lys Gln Glu Ile Thr Leu Pro Pro Ser Arg Lys Ser Glu Leu
182          595          600          605
184 gta gtt gaa gtt aag tca gat aag ctc cca gaa gag atg ggc ctc ctg 1872
185 Val Val Glu Val Lys Ser Asp Lys Leu Pro Glu Glu Met Gly Leu Leu
186          610          615          620
188 cag ggc agc agc ggt gac aag agg gct ccg gga gac cag gga gag aaa 1920
189 Gln Gly Ser Ser Gly Asp Lys Arg Ala Pro Gly Asp Gln Gly Glu Lys
190 625          630          635          640
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193 Tyr Ile Asp Leu Arg His
194          645
197 <210> SEQ ID NO: 2
198 <211> LENGTH: 646
199 <212> TYPE: PRT

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200 <213> ORGANISM: Homo sapiens
202 <400> SEQUENCE: 2
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209 Pro Glu Leu Val Glu Val Glu Val Gly Ser Thr Ala Leu Leu Lys Cys
210 35 40 45
212 Gly Leu Ser Gln Ser Gln Gly Asn Leu Ser His Val Asp Trp Phe Ser
213 50 55 60
215 Val His Lys Glu Lys Arg Thr Leu Ile Phe Arg Val Arg Gln Gly Gln
216 65 70 75 80
218 Gly Gln Ser Glu Pro Gly Glu Tyr Glu Gln Arg Leu Ser Leu Gln Asp
219 85 90 95
221 Arg Gly Ala Thr Leu Ala Leu Thr Gln Val Thr Pro Gln Asp Glu Arg
222 100 105 110
224 Ile Phe Leu Cys Gln Gly Lys Arg Pro Arg Ser Gln Glu Tyr Arg Ile
225 115 120 125
227 Gln Leu Arg Val Tyr Lys Ala Pro Glu Glu Pro Asn Ile Gln Val Asn
228 130 135 140
230 Pro Leu Gly Ile Pro Val Asn Ser Lys Glu Pro Glu Glu Val Ala Thr
231 145 150 155 160
233 Cys Val Gly Arg Asn Gly Tyr Pro Ile Pro Gln Val Ile Trp Tyr Lys
234 165 170 175
236 Asn Gly Arg Pro Leu Lys Glu Glu Lys Asn Arg Val His Ile Gln Ser
237 180 185 190
239 Ser Gln Thr Val Glu Ser Ser Gly Leu Tyr Thr Leu Gln Ser Ile Leu
240 195 200 205
242 Lys Ala Gln Leu Val Lys Glu Asp Lys Asp Ala Gln Phe Tyr Cys Glu
243 210 215 220
245 Leu Asn Tyr Arg Leu Pro Ser Gly Asn His Met Lys Glu Ser Arg Glu
246 225 230 235 240
248 Val Thr Val Pro Val Phe Tyr Pro Thr Glu Lys Val Trp Leu Glu Val
249 245 250 255
251 Glu Pro Val Gly Met Leu Lys Glu Gly Asp Arg Val Glu Ile Arg Cys
252 260 265 270
254 Leu Ala Asp Gly Asn Pro Pro Pro His Phe Ser Ile Ser Lys Gln Asn
255 275 280 285
257 Pro Ser Thr Arg Glu Ala Glu Glu Thr Thr Asn Asp Asn Gly Val
258 290 295 300
260 Leu Val Leu Glu Pro Ala Arg Lys Glu His Ser Gly Arg Tyr Glu Cys
261 305 310 315 320
263 Gln Gly Leu Asp Leu Asp Thr Met Ile Ser Leu Leu Ser Glu Pro Gln
264 325 330 335
266 Glu Leu Leu Val Asn Tyr Val Ser Asp Val Arg Val Ser Pro Ala Ala
267 340 345 350
269 Pro Glu Arg Gln Glu Gly Ser Ser Leu Thr Leu Thr Cys Glu Ala Glu
270 355 360 365
272 Ser Ser Gln Asp Leu Glu Phe Gln Trp Leu Arg Glu Thr Gly Gln

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273      370      375      380
275 Val Leu Glu Arg Gly Pro Val Leu Gln Leu His Asp Leu Lys Arg Glu
276 385      390      395      400
278 Ala Gly Gly Gly Tyr Arg Cys Val Ala Ser Val Pro Ser Ile Pro Gly
279      405      410      415
281 Leu Asn Arg Thr Gln Leu Val Asn Val Ala Ile Phe Gly Pro Pro Trp
282      420      425      430
284 Met Ala Phe Lys Glu Arg Lys Val Trp Val Lys Glu Asn Met Val Leu
285      435      440      445
287 Asn Leu Ser Cys Glu Ala Ser Gly His Pro Arg Pro Thr Ile Ser Trp
288      450      455      460
290 Asn Val Asn Gly Thr Ala Ser Glu Gln Asp Gln Asp Pro Gln Arg Val
291 465      470      475      480
293 Leu Ser Thr Leu Asn Val Leu Val Thr Pro Glu Leu Leu Glu Thr Gly
294      485      490      495
296 Val Glu Cys Thr Ala Ser Asn Asp Leu Gly Lys Asn Thr Ser Ile Leu
297      500      505      510
299 Phe Leu Glu Leu Val Asn Leu Thr Thr Leu Thr Pro Asp Ser Asn Thr
300      515      520      525
302 Thr Thr Gly Leu Ser Thr Ser Thr Ala Ser Pro His Thr Arg Ala Asn
303      530      535      540
305 Ser Thr Ser Thr Glu Arg Lys Leu Pro Glu Pro Glu Ser Arg Gly Val
306 545      550      555      560
308 Val Ile Val Ala Val Ile Val Cys Ile Leu Val Leu Ala Val Leu Gly
309      565      570      575
311 Ala Val Leu Tyr Phe Leu Tyr Lys Lys Gly Lys Leu Pro Cys Arg Arg
312      580      585      590
314 Ser Gly Lys Gln Glu Ile Thr Leu Pro Pro Ser Arg Lys Ser Glu Leu
315      595      600      605
317 Val Val Glu Val Lys Ser Asp Lys Leu Pro Glu Glu Met Gly Leu Leu
318      610      615      620
320 Gln Gly Ser Ser Gly Asp Lys Arg Ala Pro Gly Asp Gln Gly Glu Lys
321 625      630      635      640
323 Tyr Ile Asp Leu Arg His
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328-<211> LENGTH: 1960
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333 <221> NAME/KEY: CDS
334 <222> LOCATION: (8)..(1945)
336 <400> SEQUENCE: 3
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341 tgc tgc tgc tgt cct cgc gtc gcg ggt gtg ccc gga gag gct gag cag 97
342 Cys Cys Cys Cys Pro Arg Val Ala Gly Val Pro Gly Glu Ala Glu Gln
343 15      20      25      30

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VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/653,961

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number